















PR	2.1-e+21-1999;	9905-0160768;
PR	2.1-e+21-1999;	9905-0160768;
PR	2.1-e+21-1999;	9905-0160770;
PR	2.1-e+21-1999;	9905-0160814;
PR	2.1-e+21-1999;	9905-0160815;
PR	2.2-e+21-1999;	9905-0160880;
PR	2.2-e+21-1999;	9905-0160981;
PR	2.2-e+21-1999;	9905-0160989;
PR	2.5-e+21-1999;	9905-0161404;
PR	2.5-e+21-1999;	9905-0161405;
PR	2.5-e+21-1999;	9905-0161406;
PR	2.6-e+21-1999;	9905-0161459;
PR	2.6-e+21-1999;	9905-0161460;
PR	2.6-e+21-1999;	9905-0161461;
PR	2.6-e+21-1999;	9905-0161920;
PR	2.8-e+21-1999;	9905-0161992;
PR	2.8-e+21-1999;	9905-0161993;
PR	2.9-e+21-1999;	9905-0162142;

42, 98; SCORIO 1982, 4; 1982, 1; LAPOINTE 1982, 4.

Matches	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300																																																	
Concordia	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200

UNIVERSITY OF ALABAMA

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2000 2001 2002 2003 2004 2005 2006 2007 2008 2009 2010 2011 2012 2013 2014 2015 2016 2017 2018 2019 2020 2021 2022 2023 2024 2025 2026 2027 2028 2029 2030 2031 2032 2033 2034 2035 2036 2037 2038 2039 2040 2041 2042 2043 2044 2045 2046 2047 2048 2049 2050 2051 2052 2053 2054 2055 2056 2057 2058 2059 2060 2061 2062 2063 2064 2065 2066 2067 2068 2069 2070 2071 2072 2073 2074 2075 2076 2077 2078 2079 2080 2081 2082 2083 2084 2085 2086 2087 2088 2089 2090 2091 2092 2093 2094 2095 2096 2097 2098 2099 2100 2101 2102 2103 2104 2105 2106 2107 2108 2109 2110 2111 2112 2113 2114 2115 2116 2117 2118 2119 2120 2121 2122 2123 2124 2125 2126 2127 2128 2129 2130 2131 2132 2133 2134 2135 2136 2137 2138 2139 2140 2141 2142 2143 2144 2145 2146 2147 2148 2149 2150 2151 2152 2153 2154 2155 2156 2157 2158 2159 2160 2161 2162 2163 2164 2165 2166 2167 2168 2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179 2180 2181 2182 2183 2184 2185 2186 2187 2188 2189 2190 2191 2192 2193 2194 2195 2196 2197 2198 2199 2200 2201 2202 2203 2204 2205 2206 2207 2208 2209 2210 2211 2212 2213 2214 2215 2216 2217 2218 2219 2220 2221 2222 2223 2224 2225 2226 2227 2228 2229 2230 2231 2232 2233 2234 2235 2236 2237 2238 2239 2240 2241 2242 2243 2244 2245 2246 2247 2248 2249 2250 2251 2252 2253 2254 2255 2256 2257 2258 2259 2260 2261 2262 2263 2264 2265 2266 2267 2268 2269 2270 2271 2272 2273 2274 2275 2276 2277 2278 2279 2280 2281 2282 2283 2284 2285 2286 2287 2288 2289 2290 2291 2292 2293 2294 2295 2296 2297 2298 2299 2300 2301 2302 2303 2304 2305 2306 2307 2308 2309 2310 2311 2312 2313 2314 2315 2316 2317 2318 2319 2320 2321 2322 2323 2324 2325 2326 2327 2328 2329 2330 2331 2332 2333 2334 2335 2336 2337 2338 2339 2340 2341 2342 2343 2344 2345 2346 2347 2348 2349 2350 2351 2352 2353 2354 2355 2356 2357 2358 2359 2360 2361 2362 2363 2364 2365 2366 2367 2368 2369 2370 2371 2372 2373 2374 2375 2376 2377 2378 2379 2380 2381 2382 2383 2384 2385 2386 2387 2388 2389 2390 2391 2392 2393 2394 2395 2396 2397 2398 2399 2400 2401 2402 2403 2404 2405 2406 2407 2408 2409 2410 2411 2412 2413 2414 2415 2416 2417 2418 2419 2420 2421 2422 2423 2424 2425 2426 2427 2428 2429 2430 2431 2432 2433 2434 2435 2436 2437 2438 2439 2440 2441 2442 2443 2444 2445 2446 2447 2448 2449 2450 2451 2452 2453 2454 2455 2456 2457 2458 2459 2460 2461 2462 2463 2464 2465 2466 2467 2468 2469 2470 2471 2472 2473 2474 2475 2476 2477 2478 2479 2480 2481 2482 2483 2484 2485 2486 2487 2488 2489 2490 2491 2492 2493 2494 2495 2496 2497 2498 2499 2500 2501 2502 2503 2504 2505 2506 2507 2508 2509 2510 2511 2512 2513 2514 2515 2516 2517 2518 2519 2520 2521 2522 2523 2524 2525 2526 2527 2528 2529 2530 2531 2532 2533 2534 2535 2536 2537 2538 2539 2540 2541 2542 2543 2544 2545 2546 2547 2548 2549 2550 2551 2552 2553 2554 2555 2556 2557 2558 2559 2560 2561 2562 2563 2564 2565 2566 2567 2568 2569 2570 2571 2572 2573 2574 2575 2576 2577 2578 2579 2580 2581 2582 2583 2584 2585 2586 2587 2588 2589 2590 2591 2592 2593 2594 2595 2596 2597 2598 2599 2600 2601 2602 2603 2604 2605 2606 2607 2608 2609 2610 2611 2612 2613 2614 2615 2616 2617 2618 2619 2620 2621 2622 2623 2624 2625 2626 2627 2628 2629 2630 2631 2632 2633 2634 2635 2636 2637 2638 2639 2640 2641 2642 2643 2644 2645 2646 2647 2648 2649 2650 2651 2652 2653 2654 2655 2656 2657 2658 2659 2660 2661 2662 2663 2664 2665 2666 2667 2668 2669 2670 2671 2672 2673 2674 2675 2676 2677 2678 2679 2680 2681 2682 2683 2684 2685 2686 2687 2688 2689 2690 2691 2692 2693 2694 2695 2696 2697 2698 2699 2700 2701 2702 2703 2704 2705 2706 2707 2708 2709 2710 2711 2712 2713 2714 2715 2716 2717 2718 2719 2720 2721 2722 2723 2724 2725 2726 2727 2728 2729 2730 2731 2732 2733 2734 2735 2736 2737 2738 2739 2740 2741 2742 2743 2744 2745 2746 2747 2748 2749 2750 2751 2752 2753 2754 2755 2756 2757 2758 2759 2760 2761 2762 2763 2764 2765 2766 2767 2768 2769 2770 2771 2772 2773 2774 2775 2776 2777 2778 2779 2780 2781 2782 2783 2784 2785 2786 2787 2788 2789 2790 2791 2792 2793 2794 2795 2796 2797 2798 2799 2800 2801 2802 2803 2804 2805 2806 2807 2808 2809 2810 2811 2812 2813 2814 2815 2816 2817 2818

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1966, 1967, 1968, 1969, 1970, 1971, 1972, 1973, 1974, 1975, 1976, 1977, 1978, 1979, 1980, 1981, 1982, 1983, 1984, 1985, 1986, 1987, 1988, 1989, 1990, 1991, 1992, 1993, 1994, 1995, 1996, 1997, 1998, 1999, 2000, 2001, 2002, 2003, 2004, 2005, 2006, 2007, 2008, 2009, 2010, 2011, 2012, 2013, 2014, 2015, 2016, 2017, 2018, 2019, 2020, 2021, 2022, 2023, 2024, 2025, 2026, 2027, 2028, 2029, 2030, 2031, 2032, 2033, 2034, 2035, 2036, 2037, 2038, 2039, 2040, 2041, 2042, 2043, 2044, 2045, 2046, 2047, 2048, 2049, 2050, 2051, 2052, 2053, 2054, 2055, 2056, 2057, 2058, 2059, 2060, 2061, 2062, 2063, 2064, 2065, 2066, 2067, 2068, 2069, 2070, 2071, 2072, 2073, 2074, 2075, 2076, 2077, 2078, 2079, 2080, 2081, 2082, 2083, 2084, 2085, 2086, 2087, 2088, 2089, 2090, 2091, 2092, 2093, 2094, 2095, 2096, 2097, 2098, 2099, 2100, 2101, 2102, 2103, 2104, 2105, 2106, 2107, 2108, 2109, 2110, 2111, 2112, 2113, 2114, 2115, 2116, 2117, 2118, 2119, 2120, 2121, 2122, 2123, 2124, 2125, 2126, 2127, 2128, 2129, 2130, 2131, 2132, 2133, 2134, 2135, 2136, 2137, 2138, 2139, 2140, 2141, 2142, 2143, 2144, 2145, 2146, 2147, 2148, 2149, 2150, 2151, 2152, 2153, 2154, 2155, 2156, 2157, 2158, 2159, 2160, 2161, 2162, 2163, 2164, 2165, 2166, 2167, 2168, 2169, 2170, 2171, 2172, 2173, 2174, 2175, 2176, 2177, 2178, 2179, 2180, 2181, 2182, 2183, 2184, 2185, 2186, 2187, 2188, 2189, 2190, 2191, 2192, 2193, 2194, 2195, 2196, 2197, 2198, 2199, 2200, 2201, 2202, 2203, 2204, 2205, 2206, 2207, 2208, 2209, 2210, 2211, 2212, 2213, 2214, 2215, 2216, 2217, 2218, 2219, 2220, 2221, 2222, 2223, 2224, 2225, 2226, 2227, 2228, 2229, 2230, 2231, 2232, 2233, 2234, 2235, 2236, 2237, 2238, 2239, 2240, 2241, 2242, 2243, 2244, 2245, 2246, 2247, 2248, 2249, 2250, 2251, 2252, 2253, 2254, 2255, 2256, 2257, 2258, 2259, 2260, 2261, 2262, 2263, 2264, 2265, 2266, 2267, 2268, 2269, 2270, 2271, 2272, 2273, 2274, 2275, 2276, 2277, 2278, 2279, 2280, 2281, 2282, 2283, 2284, 2285, 2286, 2287, 2288, 2289, 2290, 2291, 2292, 2293, 2294, 2295, 2296, 2297, 2298, 2299, 2300, 2301, 2302, 2303, 2304, 2305, 2306, 2307, 2308, 2309, 2310, 2311, 2312, 2313, 2314, 2315, 2316, 2317, 2318, 2319, 2320, 2321, 2322, 2323, 2324, 2325, 2326, 2327, 2328, 2329, 2330, 2331, 2332, 2333, 2334, 2335, 2336, 2337, 2338, 2339, 2340, 2341, 2342, 2343, 2344, 2345, 2346, 2347, 2348, 2349, 2350, 2351, 2352, 2353, 2354, 2355, 2356, 2357, 2358, 2359, 2360, 2361, 2362, 2363, 2364, 2365, 2366, 2367, 2368, 2369, 2370, 2371, 2372, 2373, 2374, 2375, 2376, 2377, 2378, 2379, 2380, 2381, 2382, 2383, 2384, 2385, 2386, 2387, 2388, 2389, 2390, 2391, 2392, 2393, 2394, 2395, 2396, 2397, 2398, 2399, 2400, 2401, 2402, 2403, 2404, 2405, 2406, 2407, 2408, 2409, 2410, 2411, 2412, 2413, 2414, 2415, 2416, 2417, 2418, 2419, 2420, 2421, 2422, 2423, 2424, 2425, 2426, 2427, 2428, 2429, 2430, 2431, 2432, 2433, 2434, 2435, 2436, 2437, 2438, 2439, 2440, 2441, 2442, 2443, 2444, 2445, 2446, 2447, 2448, 2449, 2450, 2451, 2452, 2453, 2454, 2455, 2456, 2457, 2458, 2459, 2460, 2461, 2462, 2463, 2464, 2465, 2466, 2467, 2468, 2469, 2470, 2471, 2472, 2473, 2474, 2475, 2476, 2477, 2478, 2479, 2480, 2481, 2482, 2483, 2484, 2485, 2486, 2487, 2488, 2489, 2490, 2491, 2492, 2493, 2494, 2495, 2496, 2497, 2498, 2499, 2500, 2501, 2502, 2503, 2504, 2505, 2506, 2507, 2508, 2509, 2510, 2511, 2512, 2513, 2514, 2515, 2516, 2517, 2518, 2519, 2520, 2521, 2522, 2523, 2524, 2525, 2526, 2527, 2528, 2529, 2530, 2531, 2532, 2533, 2534, 2535, 2536, 2537, 2538, 2539, 2540, 2541, 2542, 2543, 2544, 2545, 2546, 2547, 2548, 2549, 2550, 2551, 2552, 2553, 2554, 2555, 2556, 2557, 2558, 2559, 2560, 2561, 2562, 2563, 2564, 2565, 2566, 2567, 2568, 2569, 2570, 2571, 2572, 2573, 2574, 2575, 2576, 2577, 2578, 2579, 2580, 2581, 2582, 2583, 2584, 2585, 2586, 2587, 2588, 2589, 2590, 2591, 2592, 2593, 2594, 2595, 2596, 2597, 2598, 2599, 2600, 2601, 2602, 2603, 2604, 2605, 2606, 2607, 2608, 2609, 2610, 2611, 2612, 2613, 2614, 2615, 2616, 2617, 2618, 2619, 2620, 2621, 2622, 2623, 2624, 2625, 2626, 2627, 2628, 2629, 2630, 2631, 2632, 2633, 2634, 2635, 2636, 2637, 2638, 2639, 2640, 2641, 2642, 2643, 2644, 2645, 2646, 2647, 26

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b 187 ekpblt pldodt qotoryqot qom to jclot pldp... 1188 1189 1190 1191 1192 1193 1194 1195 1196 1197 1198 1199 1200 1201 1202 1203 1204 1205 1206 1207 1208 1209 1210 1211 1212 1213 1214 1215 1216 1217 1218 1219 1220 1221 1222 1223 1224 1225 1226 1227 1228 1229 1230 1231 1232 1233 1234 1235 1236 1237 1238 1239 1240 1241 1242 1243 1244 1245 1246 1247 1248 1249 1250 1251 1252 1253 1254 1255 1256 1257 1258 1259 1260 1261 1262 1263 1264 1265 1266 1267 1268 1269 1270 1271 1272 1273 1274 1275 1276 1277 1278 1279 1280 1281 1282 1283 1284 1285 1286 1287 1288 1289 1290 1291 1292 1293 1294 1295 1296 1297 1298 1299 1300 1301 1302 1303 1304 1305 1306 1307 1308 1309 1310 1311 1312 1313 1314 1315 1316 1317 1318 1319 1320 1321 1322 1323 1324 1325 1326 1327 1328 1329 1330 1331 1332 1333 1334 1335 1336 1337 1338 1339 1340 1341 1342 1343 1344 1345 1346 1347 1348 1349 1350 1351 1352 1353 1354 1355 1356 1357 1358 1359 1360 1361 1362 1363 1364 1365 1366 1367 1368 1369 1370 1371 1372 1373 1374 1375 1376 1377 1378 1379 1380 1381 1382 1383 1384 1385 1386 1387 1388 1389 1390 1391 1392 1393 1394 1395 1396 1397 1398 1399 1400 1401 1402 1403 1404 1405 1406 1407 1408 1409 1410 1411 1412 1413 1414 1415 1416 1417 1418 1419 1420 1421 1422 1423 1424 1425 1426 1427 1428 1429 1430 1431 1432 1433 1434 1435 1436 1437 1438 1439 1440 1441 1442 1443 1444 1445 1446 1447 1448 1449 1450 1451 1452 1453 1454 1455 1456 1457 1458 1459 1460 1461 1462 1463 1464 1465 1466 1467 1468 1469 1470 1471 1472 1473 1474 1475 1476 1477 1478 1479 1480 1481 1482 1483 1484 1485 1486 1487 1488 1489 1490 1491 1492 1493 1494 1495 1496 1497 1498 1499 1500 1501 1502 1503 1504 1505 1506 1507 1508 1509 1510 1511 1512 1513 1514 1515 1516 1517 1518 1519 1520 1521 1522 1523 1524 1525 1526 1527 1528 1529 1530 1531 1532 1533 1534 1535 1536 1537 1538 1539 1540 1541 1542 1543 1544 1545 1546 1547 1548 1549 1550 1551 1552 1553 1554 1555 1556 1557 1558 1559 1560 1561 1562 1563 1564 1565 1566 1567 1568 1569 1570 1571 1572 1573 1574 1575 1576 1577 1578 1579 1580 1581 1582 1583 1584 1585 1586 1587 1588 1589 1590 1591 1592 1593 1594 1595 1596 1597 1598 1599 1600 1601 1602 1603 1604 1605 1606 1607 1608 1609 1610 1611 1612 1613 1614 1615 1616 1617 1618 1619 1620 1621 1622 1623 1624 1625 1626 1627 1628 1629 1630 1631 1632 1633 1634 1635 1636 1637 1638 1639 1640 1641 1642 1643 1644 1645 1646 1647 1648 1649 1650 1651 1652 1653 1654 1655 1656 1657 1658 1659 1660 1661 1662 1663 1664 1665 1666 1667 1668 1669 1670 1671 1672 1673 1674 1675 1676 1677 1678 1679 1680 1681 1682 1683 1684 1685 1686 1687 1688 1689 1690 1691 1692 1693 1694 1695 1696 1697 1698 1699 1700 1701 1702 1703 1704 1705 1706 1707 1708 1709 1710 1711 1712 1713 1714 1715 1716 1717 1718 1719 1720 1721 1722 1723 1724 1725 1726 1727 1728 1729 1730 1731 1732 1733 1734 1735 1736 1737 1738 1739 1740 1741 1742 1743 1744 1745 1746 1747 1748 1749 1750 1751 1752 1753 1754 1755 1756 1757 1758 1759 1760 1761 1762 1763 1764 1765 1766 1767 1768 1769 1770 1771 1772 1773 1774 1775 1776 1777 1778 1779 1780 1781 1782 1783 1784 1785 1786 1787 1788 1789 1790 1791 1792 1793 1794 1795 1796 1797 1798 1799 1800 1801 1802 1803 1804 1805 1806 1807 1808 1809 1810 1811 1812 1813 1814 1815 1816 1817 1818 1819 1820 1821 1822 1823 1824 1825 1826 1827 1828 1829 1830 1831 1832 1833 1834 1835 1836 1837 1838 1839 1840 1841 1842 1843 1844 1845 1846 1847 1848 1849 1850 1851 1852 1853 1854 1855 1856 1857 1858 1859 1860 1861 1862 1863 1864 1865 1866 1867 1868 1869 1870 1871 1872 1873 1874 1875 1876 1877 1878 1879 1880 1881 1882 1883 1884 1885 1886 1887 1888 1889 1890 1891 1892 1893 1894 1895 1896 1897 1898 1899 1900 1901 1902 1903 1904 1905 1906 1907 1908 1909 1910 1911 1912 1913 1914 1915 1916 1917 1918 1919 1920 1921 1922 1923 1924 1925 1926 1927 1928 1929 1930 1931 1932 1933 1934 1935 1936 1937 1938 1939 1940 1941 1942 1943 1944 1945 1946 1947 1948 1949 1950 1951 1952 1953 1954 1955 1956 1957 1958 1959 1960 1961 1962 1963 1964 1965 1966 1967 1968 1969 1970 1971 1972 1973 1974 1975 1976 1977 1978 1979 1980 1981 1982 1983 1984 1985 1986 1987 1988 1989 1990 1991 1992 1993 1994 1995 1996 1997 1998 1999 2000 2

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34 / 1PK 8PT 8T 8ST 1M9 1W5 2W 3W 4W 5W 6W 7W 8W 9W 10W 11W 12W 13W 14W 15W 16W 17W 18W 19W 20W 21W 22W 23W 24W 25W 26W 27W 28W 29W 30W 31W 32W 33W 34W 35W 36W 37W 38W 39W 40W 41W 42W 43W 44W 45W 46W 47W 48W 49W 50W 51W 52W 53W 54W 55W 56W 57W 58W 59W 60W 61W 62W 63W 64W 65W 66W 67W 68W 69W 70W 71W 72W 73W 74W 75W 76W 77W 78W 79W 80W 81W 82W 83W 84W 85W 86W 87W 88W 89W 90W 91W 92W 93W 94W 95W 96W 97W 98W 99W 100W 101W 102W 103W 104W 105W 106W 107W 108W 109W 110W 111W 112W 113W 114W 115W 116W 117W 118W 119W 120W 121W 122W 123W 124W 125W 126W 127W 128W 129W 130W 131W 132W 133W 134W 135W 136W 137W 138W 139W 140W 141W 142W 143W 144W 145W 146W 147W 148W 149W 150W 151W 152W 153W 154W 155W 156W 157W 158W 159W 160W 161W 162W 163W 164W 165W 166W 167W 168W 169W 170W 171W 172W 173W 174W 175W 176W 177W 178W 179W 180W 181W 182W 183W 184W 185W 186W 187W 188W 189W 190W 191W 192W 193W 194W 195W 196W 197W 198W 199W 200W 201W 202W 203W 204W 205W 206W 207W 208W 209W 210W 211W 212W 213W 214W 215W 216W 217W 218W 219W 220W 221W 222W 223W 224W 225W 226W 227W 228W 229W 230W 231W 232W 233W 234W 235W 236W 237W 238W 239W 240W 241W 242W 243W 244W 245W 246W 247W 248W 249W 250W 251W 252W 253W 254W 255W 256W 257W 258W 259W 260W 261W 262W 263W 264W 265W 266W 267W 268W 269W 270W 271W 272W 273W 274W 275W 276W 277W 278W 279W 280W 281W 282W 283W 284W 285W 286W 287W 288W 289W 290W 291W 292W 293W 294W 295W 296W 297W 298W 299W 300W 301W 302W 303W 304W 305W 306W 307W 308W 309W 310W 311W 312W 313W 314W 315W 316W 317W 318W 319W 320W 321W 322W 323W 324W 325W 326W 327W 328W 329W 330W 331W 332W 333W 334W 335W 336W 337W 338W 339W 340W 341W 342W 343W 344W 345W 346W 347W 348W 349W 350W 351W 352W 353W 354W 355W 356W 357W 358W 359W 360W 361W 362W 363W 364W 365W 366W 367W 368W 369W 370W 371W 372W 373W 374W 375W 376W 377W 378W 379W 380W 381W 382W 383W 384W 385W 386W 387W 388W 389W 390W 391W 392W 393W 394W 395W 396W 397W 398W 399W 400W 401W 402W 403W 404W 405W 406W 407W 408W 409W 410W 411W 412W 413W 414W 415W 416W 417W 418W 419W 420W 421W 422W 423W 424W 425W 426W 427W 428W 429W 430W 431W 432W 433W 434W 435W 436W 437W 438W 439W 440W 441W 442W 443W 444W 445W 446W 447W 448W 449W 450W 451W 452W 453W 454W 455W 456W 457W 458W 459W 460W 461W 462W 463W 464W 465W 466W 467W 468W 469W 470W 471W 472W 473W 474W 475W 476W 477W 478W 479W 480W 481W 482W 483W 484W 485W 486W 487W 488W 489W 490W 491W 492W 493W 494W 495W 496W 497W 498W 499W 500W 501W 502W 503W 504W 505W 506W 507W 508W 509W 510W 511W 512W 513W 514W 515W 516W 517W 518W 519W 520W 521W 522W 523W 524W 525W 526W 527W 528W 529W 530W 531W 532W 533W 534W 535W 536W 537W 538W 539W 540W 541W 542W 543W 544W 545W 546W 547W 548W 549W 550W 551W 552W 553W 554W 555W 556W 557W 558W 559W 560W 561W 562W 563W 564W 565W 566W 567W 568W 569W 570W 571W 572W 573W 574W 575W 576W 577W 578W 579W 580W 581W 582W 583W 584W 585W 586W 587W 588W 589W 590W 591W 592W 593W 594W 595W 596W 597W 598W 599W 600W 601W 602W 603W 604W 605W 606W 607W 608W 609W 610W 611W 612W 613W 614W 615W 616W 617W 618W 619W 620W 621W 622W 623W 624W 625W 626W 627W 628W 629W 630W 631W 632W 633W 634W 635W 636W 637W 638W 639W 640W 641W 642W 643W 644W 645W 646W 647W 648W 649W 650W 651W 652W 653W 654W 655W 656W 657W 658W 659W 660W 661W 662W 663W 664W 665W 666W 667W 668W 669W 670W 671W 672W 673W 674W 675W 676W 677W 678W 679W 680W 681W 682W 683W 684W 685W 686W 687W 688W 689W 690W 691W 692W 693W 694W 695W 696W 697W 698W 699W 700W 701W 702W 703W 704W 705W 706W 707W 708W 709W 710W 711W 712W 713W 714W 715W 716W 717W 718W 719W 720W 721W 722W 723W 724W 725W 726W 727W 728W 729W 730W 731W 732W 733W 734W 735W 736W 737W 738W 739W 740W 741W 742W 743W 744W 745W 746W 747W 748W 749W 750W 751W 752W 753W 754W 755W 756W 757W 758W 759W 760W 761W 762W 763W 764W 765W 766W 767W 768W 769W 770W 771W 772W 773W 774W 775W 776W 777W 778W 779W 780W 781W 782W 783W 784W 785W 786W 787W 788W 789W 790W 791W 792W 793W 794W 795W 796W 797W 798W 799W 800W 801W 802W 803W 804W 805W 806W 807W 808W 809W 810W 811W 812W 813W 814W 815W 816W 817W 818W 819W 820W 821W 822W 823W 824W 825W 826W 827W 828W 829W 830W 831W 832W 833W 834W 835W 836W 8

**Hoffmann, David Paul** b.1970  
M.D.

$A(A) = \{a, b, c, d, e, f, g, h, i, j, k, l, m, n, o, p, q, r, s, t, u, v, w, x, y, z\}$

188 SWAT ENVIRONMENTAL DATA CENTER, 1000 N. MEVILLY AVE.,

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AG512H9

18-061-2000 (first entry)

*Arabidopsis thaliana* protein fragment S101b-N1: 61,080.



XX Protein identification: signal transduction pathway: metabolic pathway  
 KW hybridization assay: protein: maffin1 gene expression: metabolic: promoter  
 KW termination sequence  
 XX  
 XX Arabidopsis thaliana  
 PN EPI03405 A2  
 XX  
 XX  
 ED 06-SEP-2000  
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Score

100%

100%

100%

100%

## Host Label Similarity

44.8%

Score

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100%

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100%

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Mismatches

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## CY

144

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SA

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## DB

144

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Job time: 194 sec

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1  
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3



[illegible]
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1 SOFTWARE: Patent In Release #1.0, Version #1.00  
 2 CURRENT APPLICATION DATA:  
 3 APPLICANT: RUSK, LARS  
 4 FILING DATE: 19-APR-1996  
 5 CLASSIFICATION: 800  
 6 ATTORNEY/AGENT INFORMATION:  
 7 NAME: Smith, William M.  
 8 REGISTRATION NUMBER: 30,223  
 9 REFERENCE/PRIOR ART INFORMATION:  
 10 PUBLICATION NO. 1,234,567  
 11 TELEPHONE: (415) 576-0200  
 12 TELEFAX: (415) 576-0400  
 13 INFORMATION ISR SEQ. ID. NO. 2:  
 14 SEQUENCE CHARACTERISTICS:  
 15 LENGTH: 506 amino acids  
 16 TYPE: amino acid  
 17 TOPOLOGY: linear  
 18 MOLECULE TYPE: protein  
 19 OR 645,066-2

Query Match: 40.28; Score 1015.4; DB 2; Length 506;

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 200 A S P A R T A M I N O A C I D S

1 APPLICANT: Rusk, Lars  
 2 APPLICANT: Gromley, George R.  
 3 APPLICANT: Murray, Edward M.  
 4 APPLICANT: Human, Goran  
 5 TITLE OF INVENTION: Human Collection Sensor Protein, Polymers  
 6 NUMBER OF SEQUENCES: 84  
 7 CORRESPONDENCE ADDRESS:  
 8 ADDRESS: Martin Savitzky  
 9 STREET: Rhine-Poulton Road, Box 500, Arcadia, CA 91006  
 10 STREET: 8043  
 11 CITY: Glendale, CA 91206  
 12 STATE: CA  
 13 COUNTRY: USA  
 14 ZIP: 91206-0107  
 15 COMPUTER READABLE FORM:  
 16 MEDIUM TYPE: floppy disk  
 17 OPERATING SYSTEM: Windows 95  
 18 SOFTWARE: Word 7.0 (Patent In)  
 19 CURRENT APPLICATION DATA:  
 20 APPLICATION NUMBER: 09-08-576-778-10  
 21 FILING DATE: 07 JUN-1995  
 22 CLASSIFICATION: 405  
 23 PRIOR APPLICATION DATA:  
 24 APPLICATION NUMBER: 09-08-576-778-10  
 25 FILING DATE: 28 MAY-1994  
 26 PRIOR APPLICATION DATA:  
 27 APPLICATION NUMBER: 09-08-576-778-10  
 28 FILING DATE: 28 MAY-1994  
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 84 FILLING DATE: 28 MAY-1994







1 Portlet No. 618/548  
 2 GENERAL INFORMATION:  
 3 APPLICANT: Abstract, Aaron  
 4 APPLICANT: Public, Claus  
 5 APPLICANT: Kask, Lars  
 6 APPLICANT: Crowley, Gregg R.  
 7 APPLICANT: Morris, Edward M.  
 8 APPLICANT: Murray, Edward M.  
 9 APPLICANT: Huling, Brian  
 10 TITLE OF INVENTION: Human Calcium Sensor, Protein, Fragments  
 11 TITLE OF INVENTION: The Food and Drug Administration  
 12 NUMBER OF SEQUENCES: 106  
 13 CORRESPONDENCE ADDRESS:  
 14 ADDRESS: Rhode-Island Rotor Inc.  
 15 STREET: 500 Arcola Rd., 0644  
 16 CITY: Collosoville  
 17 STATE: PA  
 18 COUNTRY: USA  
 19 ZIPS: 19426-0707  
 20 COMPUTER READABLE FORM:  
 21 MEDIUM TYPE: Floppy disk  
 22 COMPUTER: Macintosh  
 23 OPERATING SYSTEM: System 7.5.1  
 24 SOFTWARE: Word 5.0 (Patented)  
 25 CURRENT APPLICATION DATA:  
 26 INVENTOR NUMBER: 05/09/97/2,877  
 27 FILING DATE:  
 28 CLASSIFICATION: 4.45  
 29 PRIOR APPLICATION DATA:  
 30 APPLICATION NUMBER: 101/0037/15,204  
 31 FILING DATE: 22 Nov 1995  
 32 PRIOR APPLICATION DATA:  
 33 APPLICATION NUMBER: 05/09/94/846  
 34 FILING DATE: 24 Nov 1994  
 35 PRIOR APPLICATION DATA:  
 36 APPLICATION NUMBER: 05/08/87/414  
 37 FILING DATE: 07 JUNE 1995  
 38 ATTORNEY/AGENT INFORMATION:  
 39 NAME: SATLECK, Martin  
 40 REGISTRATION NUMBER: 29,699  
 41 REFERENCE/WORK NUMBER: A1355C-05  
 42 TELECOMMUNICATION INFORMATION:  
 43 TELEPHONE: 610-454-4816  
 44 TELEFAX: 610-454-4808  
 45 INFORMATION FOR SEQ ID NO: 86:  
 46 SEQUENCE CHARACTERISTICS:  
 47 LENGTH: 4655 amino acids  
 48 TYPE: amino acid  
 49 FEATURE: linear  
 50 MULTIPLE TYPE: Protein  
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Post-Local Similarity: 54.38; Pred. No. 2,5025;  
 ModChes: 276; Conservative: 59; Mismatches: 90;  
 Indels: 83; Gaps: 46.

[illegible]

## References

amino acid 1,4-oxanuranose (EC 3.2.1.7) Celvex precursor - Clostridium cellulolyticum  
 C:Species: Clostridium cellulolyticum  
 C:Date: 30 Sep 1992 sequence revision to Sep 1993 (text change 21-Jul-2000  
 C:Accession: jcl400  
 K:Barakat-Tardif, C.; Gaudin, C.; Melachy, A.; Hoest, P.; Clard, T.; Melachy, J.P.,  
 Gene 119, 17-19, 1992  
 A:Title: Sequence analysis of a gene cluster encoding cellulases from Clostridium cellu  
 A:Accession number: jcl1299; M010:94012971  
 A:Accession: jcl400  
 A:Molecule type: rRNA  
 A:Accession: J 725, rNA  
 A:Cross references: GI:3667018; N10:q5597001; P10N:AA71866.1; P10:q551774  
 C:Notes:  
 A:Notes: cell303  
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 C:Keywords: glycosidase; hydrolase  
 E:1-45/Name: signal sequence #stems Predicted <310  
 E:1-45/2/Product: endo-beta-1,4-glucanase Celvex #stems Predicted <MAT-  
 E:664-687/Name: clostridium cellulase repeat hemology #882  
 E:696-719/Name: clostridium cellulase repeat hemology #882  
 E:90-94,160,408,455,760-760,516,567,587,619,639,659,679,699,719,739,759,779,799,819,839,859,879,899,919,939,959,979,999,1019,1039,1059,1079,1099,1119,1139,1159,1179,1199,1219,1239,1259,1279,1299,1319,1339,1359,1379,1399,1419,1439,1459,1479,1499,1519,1539,1559,1579,1599,1619,1639,1659,1679,1699,1719,1739,1759,1779,1799,1819,1839,1859,1879,1899,1919,1939,1959,1979,1999,2019,2039,2059,2079,2099,2119,2139,2159,2179,2199,2219,2239,2259,2279,2299,2319,2339,2359,2379,2399,2419,2439,2459,2479,2499,2519,2539,2559,2579,2599,2619,2639,2659,2679,2699,2719,2739,2759,2779,2799,2819,2839,2859,2879,2899,2919,2939,2959,2979,2999,3019,3039,3059,3079,3099,3119,3139,3159,3179,3199,3219,3239,3259,3279,3299,3319,3339,3359,3379,3399,3419,3439,3459,3479,3499,3519,3539,3559,3579,3599,3619,3639,3659,3679,3699,3719,3739,3759,3779,3799,3819,3839,3859,3879,3899,3919,3939,3959,3979,3999,4019,4039,4059,4079,4099,4119,4139,4159,4179,4199,4219,4239,4259,4279,4299,4319,4339,4359,4379,4399,4419,4439,4459,4479,4499,4519,4539,4559,4579,4599,4619,4639,4659,4679,4699,4719,4739,4759,4779,4799,4819,4839,4859,4879,4899,4919,4939,4959,4979,4999,5019,5039,5059,5079,5099,5119,5139,5159,5179,5199,5219,5239,5259,5279,5299,5319,5339,5359,5379,5399,5419,5439,5459,5479,5499,5519,5539,5559,5579,5599,5619,5639,5659,5679,5699,5719,5739,5759,5779,5799,5819,5839,5859,5879,5899,5919,5939,5959,5979,5999,6019,6039,6059,6079,6099,6119,6139,6159,6179,6199,6219,6239,6259,6279,6299,6319,6339,6359,6379,6399,6419,6439,6459,6479,6499,6519,6539,6559,6579,6599,6619,6639,6659,6679,6699,6719,6739,6759,6779,6799,6819,6839,6859,6879,6899,6919,6939,6959,6979,6999,7019,7039,7059,7079,7099,7119,7139,7159,7179,7199,7219,7239,7259,7279,7299,7319,7339,7359,7379,7399,7419,7439,7459,7479,7499,7519,7539,7559,7579,7599,7619,7639,7659,7679,7699,7719,7739,7759,7779,7799,7819,7839,7859,7879,7899,7919,7939,7959,7979,7999,8019,8039,8059,8079,8099,8119,8139,8159,8179,8199,8219,8239,8259,8279,8299,8319,8339,8359,8379,8399,8419,8439,8459,8479,8499,8519,8539,8559,8579,8599,8619,8639,8659,8679,8699,8719,8739,8759,8779,8799,8819,8839,8859,8879,8899,8919,8939,8959,8979,8999,9019,9039,9059,9079,9099,9119,9139,9159,9179,9199,9219,9239,9259,9279,9299,9319,9339,9359,9379,9399,9419,9439,9459,9479,9499,9519,9539,9559,9579,9599,9619,9639,9659,9679,9699,9719,9739,9759,9779,9799,9819,9839,9859,9879,9899,9919,9939,9959,9979,9999,10019,10039,10059,10079,10099,10119,10139,10159,10179,10199,10219,10239,10259,10279,10299,10319,10339,10359,10379,10399,10419,10439,10459,10479,10499,10519,10539,10559,10579,10599,10619,10639,10659,10679,10699,10719,10739,10759,10779,10799,10819,10839,10859,10879,10899,10919,10939,10959,10979,10999,11019,11039,11059,11079,11099,11119,11139,11159,11179,11199,11219,11239,11259,11279,11299,11319,11339,11359,11379,11399,11419,11439,11459,11479,11499,11519,11539,11559,11579,11599,11619,11639,11659,11679,11699,11719,11739,11759,11779,11799,11819,11839,11859,11879,11899,11919,11939,11959,11979,11999,12019,12039,12059,12079,12099,12119,12139,12159,12179,12199,12219,12239,12259,12279,12299,12319,12339,12359,12379,12399,12419,12439,12459,12479,12499,12519,12539,12559,12579,12599,12619,12639,12659,12679,12699,12719,12739,12759,12779,12799,12819,12839,12859,12879,12899,12919,12939,12959,12979,12999,13019,13039,13059,13079,13099,13119,13139,13159,13179,13199,13219,13239,13259,13279,13299,13319,13339,13359,13379,13399,13419,13439,13459,13479,13499,13519,13539,13559,13579,13599,13619,13639,13659,13679,13699,13719,13739,13759,13779,13799,13819,13839,13859,13879,13899,13919,13939,13959,13979,13999,14019,14039,14059,14079,1

Quarter Match	58.48;	Scores	1474.8;	DB 2;	Length	725
Post	1004	Simultaneous	40	98;	Prod	6.5026

Matches 274; Conservative 72; Mismatches 82; Indels 242; Gaps 45.

[illegible][illegible]

01	02	03	04	05	06	07	08	09	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99
01	02	03	04	05	06	07	08	09	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99
01	02	03	04	05	06	07	08	09	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99
01	02	03	04	05	06	07	08	09	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99
01	02	03	04	05	06	07	08	09	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99
01	02	03	04	05	06	07	08	09	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85														

## RESULTS

Cellobiose (EC 2.1.4) E precursor - chloridium thermophilum  
N-Alternate names: endo-1,4-beta-cellulose  
C Species: Chloridium thermophilum  
ClDate: 12-Mar-1993 #sequence\_revision 12-Mar-1993 next change 15-Oct-1999  
C Accession: S15727  
R Navarro, A.; Chedon, M.<sup>1</sup>; Benin, P.; Aubert, J.P.,  
submitted to the EMBL Data Library, July 1991  
A Description: Nucleotide sequence of the cellobiose gene cglB of chloridium thermophilum  
A Reference number: S15727  
A Accession: S15727  
A Molecule type: DNA  
A Keywords: 1739 NAV  
A Cross references: EMBL X05675, NIH 343677, FIMB ZAA 00011, DDBJ 011006  
A Experimental source: NCIB 10582  
C Genes/cds:  
A Gene: cglF  
A Start codon: TTG  
C Function:  
A Description: hydrolysis of 1,4 beta-D-glucosidic linkages in beta-D-glucans such as  
A Pathway: cellulose degradation  
C Superfamily: chloridium cellobiose repeat homology  
C Keywords: extracellular protein glycosylase; hydrolytic polysaccharide debrancher  
E 1-27/Alanine signal sequence; astars predicted - SDP  
E 1-28-739/predicted; cyclization; E status predicted - MAI  
E 670-693/Alanine; chloridium cellobiose repeat homology - YKJ  
Y 709-742/Alanine; chloridium cellobiose repeat homology - YKJ



[illegible]



[illegible][illegible]

Wed Mar 6 06:50:57 2002

us-09-576-778-10\_copy\_26\_485.mar5.rpr

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RESULT 4  
GUNA VASA  
ID GUNA VASA STANDARD PRT: 1742 AA  
AC P22543  
DI 01 AUG-1991 (REL. 19, Created)  
DI 01 OCT-1996 (REL. 34, Last sequence update)  
DI 15-JUL-1998 (REL. 46, Last annotation update)  
DE ENDOLUCANASE A (FBI-1,2,1,4) (FBI-1,4 beta glucanase A)  
EN CELLA  
SS Calabellum saccharolyticum (Calabellum streptococcus saccharolyticus)  
AC Bacteria: Firmicutes; Bacillus/Clostridium group  
AC Bacteroidetes group; Clostridiaceae group  
X NCBI TaxID 441017  
X 111  
X SEQUENCE FROM N.A.  
X MEDLINE 95346703; PubMed 7612247;  
X Leu V.S., Saul D.J., Jeppan P.L.;  
X "Cella, another group coding for a multi-domain cellulase from the  
X extreme thermophilic Calabellum saccharolyticum";  
X Appl. Microbiol. Biotechnol. 43:291-296(1995).  
X 121  
X SEQUENCE OF 1516 1742 FROM N.A  
X MEDLINE 91247819; PubMed 2039240;  
X Leubti E., Jansat N.R., Grayling R.A., Lope D.R., Jeppan P.L.;  
X "Cloning, sequence analysis, and expression in Escherichia coli of a  
X bacterium Calabellum saccharolyticum";  
X Appl. Environ. Microbiol. 57:694-700(1991).  
X 1  
X FUNCTION: THE N-TERMINAL DOMAIN OF CELLA ENCODES FOR AN  
X ENDOLUCANASE ACTIVITY ON CARBOHYDRATE POLYSACCHARIDES.  
X DOMAIN PROBABLY ACT SYNERGISTICALLY TO HYDROLYZE CRYSTALLINE  
X CELLULOSE.  
X 1  
X CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-GLUCOSIDIC  
X LINKAGES IN CELLULOSE.  
X 1  
X THE LINEAR SECTON (ALSO TERMED "HINCE") MAY BE A POTENTIAL  
X SITE FOR PROTEOLYSIS  
X 1  
X SIMILARITY: IN THE N-TERMINAL SECTON, RELIGIONS TO CELLULOSE FAMILY  
X E (FAMILY 9 OF GLYCOSYL HYDROLASES).  
X 1  
X SIMILARITY: IN THE C-TERMINAL SECTON, RELIGIONS TO CELLULOSE FAMILY  
X I (FAMILY 46 OF GLYCOSYL HYDROLASES).  
X 1  
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X between the Swiss Institute of Bioinformatics and the EMBL Outstation  
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X or send an email to license@ebi.ac.uk).

RESULT 5  
GUNA VASA  
ID GUNA VASA STANDARD PRT: 986 AA  
AC P24659  
DI 01-NOV-1991 (REL. 20, Created)  
DI 01-NOV-1991 (REL. 20, Last sequence update)  
DI 15-JUL-1998 (REL. 46, Last annotation update)  
DE ENDOLUCANASE A (FBI-1,2,1,4) (FBI-1,4 beta glucanase A)  
EN CELLA  
SS Calabellum saccharolyticum  
AC Bacteria: Firmicutes; Bacillus/Clostridium group; Clostridiaceae  
AC Clostridium  
X NCBI TaxID 15107  
X 111  
X SEQUENCE FROM N.A. AND SEQUENCE OF 26 46 AND 475 496.  
X STRAIN-NR111745;  
X MEDLINE 91066838; PubMed 2250552;  
X Jais S., Roca-Knapel K.L., Schwach W.H., Knäuper P.;  
X "Domain-act K. Staudenmann W.L.;"  
X "Sequence analysis of the Clostridium staudenmannii only gene encoding



[illegible]

CC bacterium/Eliminates; bacillus/clostridium group; clostridiaceae;  
CC  
CX NCB\_L018719;  
CX [1]  
RX SEQUENCE FROM N.A.  
RX STRAIN NCIM 10682;  
RX MEDLINE 92214263; PubMed 1955407;  
KA Navarro A.; Chobron M.-C.; Rouquié P.; Albert J.P.;  
RI "Nucleotide sequence of the cellulase gene cglA of Clostridium  
RI thermocellum."  
KL Nos.: Medline(1); 142727-946(1991).  
KL [2]  
RP SEQUENCE OF 1.4 FROM N.A.  
RP cglA/Nr\_00662;  
RX MEDLINE 91100422; PubMed 1987437;  
RX Medina S.; Rouquié P.; Albert J.P.;  
RI "Transcription of Clostridium thermocellum endoglucanase genes cglB  
RI and cglD."  
RL J. Bacteriol. 173:80-85(1991).  
CC  
CC 1. CELLULOSE-BINDING DOMAINS IN THE C-TERMINAL 1.4 FROM  
CC GLUCONIC ACID-LINKED CELLULOSE, LIGNIN AND TRICALBIOLAN  
CC SUBSTRATES.  
CC  
CC -I- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4 BETA-D-GLUCOSIDE  
CC LINKAGES IN CELLULOSE.  
CC  
CC -II- COFACTOR: ZINC ION.  
CC "cglA": A 1,100 AA PROTEIN WITH AN UNUSUAL HIGH AS  
CC WELL AS IN OTHER C-TERMINAL CELLULOSE DEGRADING ENZYMES THAT FORMIN  
CC RAY EFFECTS ON THE BINDING TO CELLULOSE AND TO OTHER POLYMER  
CC -I- SIMILARITY: BELONGS TO CELLULASE FAMILY II (FAMILY 9 OF GLOSTYL  
CC HYDROLASES).

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CC EMBL: X63515; GenBank: F01511;  
CC  
CC FRK: S15727; S15727;  
CC BSS: 15221; 3TP4;  
CC InterPro: IP0002105; DocKey: In 1;  
CC InterPro: IP0002048; EF-hand  
CC InterPro: IP001701; Glyco\_hydro\_9;  
CC Pfam: PF00494; DocKey: In 1; 2;  
CC Pfam: PF00759; Glyco\_hydro\_9; 1;  
CC Prosite: PS00448; CLUSTAL: SCEN\_001;  
CC Prosite: PS00448; CLUSTAL: SCEN\_001; 2;  
CC Prosite: PS00592; Glycosyl\_Hydrol\_9; 1; 1;  
CC Prosite: PS00598; Glycosyl\_Hydrol\_Py\_2; 1;  
CC Cellulose degradation; hydrolases; glycosidases; beta-d; starch;  
CC Cellulose-binding;  
CC KW SIGNAL; 1; 27  
CC FT CHAIN; 28; 749; ENDOGLUCANASE P;  
CC FT --RA--; 28; 749; ACTIVITY;  
CC FT DOMAIN; 505; 648; CELLULOSE BINDING;  
FT D086IN; 670; 742; 2 X 24 AA APPROXIMATE REPEATS;  
FT REPEAT; 709; 742; 1;  
FT REPEAT; 709; 742; 2;  
FT ACT\_SITE; 400; 400; BY SIMILARITY;  
FT ACT\_SITE; 438; 438; BY SIMILARITY;  
FT ACT\_SITE; 447; 447; BY SIMILARITY;  
SQ SOURCE; 749 AA; 92388 MW; 107480P/60DADEP; chr10:14;









1	CHARACTER	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1</
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[illegible]

[illegible][illegible]





[illegible][illegible]









1 VARIANT 487 487 1 - A  
2 VARIANT 4842 4842 R - S  
30 SEQUENCE 4898 AA 448570 MB 2011788A5040076 070544

Query Match: 49 583 Score 968 57 100 12 Length 38983

Best Local Similarity: 49 788 EVD: 26.23 137

Matches: 4287 Conserved: 467 Mismatches: 541 Indels: 26152 Gaps: 223

QY 1 AS-----AE-----EPH-----N-----Y-----10  
DB 702 SSINELISAAALITIMKYSIRIGLIGYKAVTASSTVTAIVNSPTLASLIER 761  
QY 11 A-----ELI-----Q-----K-----SIL-----PY-----21  
DB 762 ALFEVTELLTETIMALIMHEDGVDGDTGDSVAKSYNTLILNGAFYLVPIG 821  
QY 22 --E-A-----Q-----RGR--LP-----E-----NSKI--NW--R-48  
DB 822 WIGVVAIVASSTILITKLVKTER--KGTTHKAVYIIVERTKCHKQSNWVW 879  
QY 49 QDS-----GL-----E-----DQ-----46  
DB 880 GHVYKQGVKQVQKQWQTEPEKRPVGLHYRGLTINHYEVNSSTGNSQVYVST 939  
QY 47 -----KDY-----49  
DB 943 EHHHGLSHTYVEMHEDKATMECHRYVNSLQVSLTTHDLELHDEYEDR 999  
QY 50 --G-----LQI-----OG--W-----Y-----D--59  
DB 1000 HSYEVGYMKQGVWYVNLDTDHITPAFVVLVVAALLAGRVMLIYIILIDOL 1059  
QY 60 A-----D-----H-----X-----65  
DB 1060 AALQVQGVVVLISHLTHREVVYVLELVTEHELEHMLLEHMLNSQVYVTL 1119  
QY 66 -----F-----GL-----PM-----70  
DB 1120 VAVNGLSVARVYVTLWLELVTEHVSALAVVYVYVLLAKNPTLITLVYVAT 1179  
QY 71 A-----Y-----SAALISMS-V-----YFY-----84  
DB 1180 TETAKTTHHSHLVYVSAALLMTLSAATNINQGVYVSLGTHLVNLNGE 1239  
QY 85 -----R-----D-----86  
DB 1240 LHLHAPLISHGLEPYHVLISAVVLRWNLVAGLLQCVPLHWEFMWADLILIL 1299  
QY 87 -----A-----YK-----E-----S-Q-----92  
DB 1400 LPTTHLKYVYVYVTLAENQMLNPTREYVQVYVYVQVLSHVSITRSKTSATIS 1459  
QY 94 -----QI-----D-----AAL-----98  
DB 1460 TMLPLEALISSTSHWQVTLVLLFVSAYLGEVYHJAGVYVSRVMAVHLVH 1419  
QY 99 DN-----LK-----WAD--Y-----ELKA-----111  
DB 1420 KATQNVKQKKEETTLVSVVTLTKQVSVYVYVWQVTELYTMEELVEVAALIS 1479  
QY 112 --H-----LAP-----Y-----116  
DB 1480 KRRHTLVYVTEGKQKQKTRKQKQVYVYVYVYVYVYVYVYVYVYVYVYV 1549  
QY 117 E-----L-W-Q-----WGN-----VALDHAW--QVA-----145  
DB 1540 EHHAVYLYEALVTEHMLYVAVYVYVYVYVYVYVYVYVYVYVYVYVYVYV 1599  
QY 136 E-----VMYKR-----P-----AY-----145  
DB 1600 HBEGLTISIMKILAFVWVP--KGLTHRAVYRPTSLIKRKALFETQWATYHQQGISVD 1657

QY 146 -----KIDQVQVQNS-----LDAI 158  
DB 1658 HAVQGLVAVYV 1717  
QY 159 -----GIAA-----162  
DB 1718 EYDVAVYV 1777  
QY 163 -----A-----LAS A-----SII-----170  
DB 1738 FTEHMLVYV 1847  
QY 171 -----F--K-P-I-----D-----SSY-----SEKI 182  
DB 1838 RVLVLLHRAAHSVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYV 1897  
QY 184 LA-----H A KQI-----189  
DB 1898 KAAWYV 1947  
QY 190 -----Y-D-----F-----AIE-----196  
DB 1958 FIAPEVYV 2017  
QY 196 YRQK-----Y-----S-----D-----204  
DB 2018 YSDEPSSNLEVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYV 2077  
QY 204 -----T-----D-----AQQ-----210  
DB 2078 GEPKAVYV 2147  
QY 211 -----YNS-----214  
DB 2149 GEPHETIMATHEHSHMLTGLTLLNLLSHMLMAKNTMAHLLHLELAVNYVY 2197  
QY 214 -----W-----214  
DB 2196 GAVLTKLENDVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYV 2257  
QY 215 -----S-----Q-----216  
DB 2258 GVEVNAKALVY 2317  
QY 217 -----YK-----218  
DB 2418 GVAHNALEPTEVTEHFTLQGVYVYVYVYVYVYVYVYVYVYVYVYVYVY 2477  
QY 219 -----E-LI-----WLA-----VWL-----228  
DB 2478 YVAVYV 2547  
QY 229 -----YLA-----HEDDQ-----Y-----LQK 240  
DB 2478 TSEHFCZALVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYV 2497  
QY 241 --ALA-----SV-----SWQ-----249  
DB 2498 IVEPALATIDAKALSLFATRLSVVHLSATAYVYVYVYVYVYVYVYVYVY 2558  
QY 250 -----F-----251  
DB 2557 IMEGNVY 2616  
QY 252 -----A--NRP-----YR-W-----11-----260  
DB 2612 LMAFLAVYV 2675  
QY 264 -----SM-----10-----264  
DB 2676 STEKAGVYV 2735  
QY 265 V T-----Y-----GAOL-LLA-----KLI NO SPEVRS 285

[illegible]

Search completed: March 5, 2002, 08:00:31  
Job Time: 203 sec



GenCode version 4.5  
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OM Protein: Protein search, using SW model

Run on: March 5, 2002, 07:56:34, Search time 28.71 seconds  
(without alignments)  
211,172 Million cell updates/sec

Title: US-09-576-778-10\_Copy\_26\_485  
Perfect score: 2525  
Sequence: 1 ASAFYRHWATLQFSLIP VAFHLLQFSAVHLLQFSLIP

Scoring table: HSPDMS62  
Gapop 3.0, Gapext 0.1

Searches: 47695 seqs, 1462729 residues

Total number of hits satisfying chosen parameters: 473705

Minimum hit seq length: 0  
Maximum hit seq length: 2000000000

Post processing: Minimum Match: 0%  
Maximum Match: 100%

Listing first 45 summaries

Database: 1: SPKEMBL\_17: \*  
2: SP\_Archaea: \*  
3: SP\_Bacteria: \*  
4: SP\_Fungi: \*  
5: SP\_Invertebrates: \*  
6: SP\_Mammals: \*  
7: SP\_Other: \*  
8: SP\_Ctenophora: \*  
9: SP\_Phiagea: \*  
10: SP\_Plants: \*  
11: SP\_Protozoa: \*  
12: SP\_Viruses: \*  
13: SP\_Vertebrates: \*  
14: SP\_Unclassified: \*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2173.8	86.1	65	2	Q9B022	Q9B022 copiotermes
2	1994.4	75.0	65	2	Q9B016	Q9B016 bacillus p
3	1757.2	59.6	937	2	Q9A311	Q9A311 bacillus sp
4	1626.5	54.4	847	2	Q9A318	Q9A318 clostridium
5	1501.9	59.5	1711	2	P96311	P96311 anaerobell
6	1465.2	58.0	715	2	Q65987	Q65987 clostridium
7	1410.8	55.9	1751	2	Q9A004	Q9A004 bacillus p
8	1356.5	54.7	742	2	Q9B345	Q9B345 clostridium
9	1355.4	52.9	737	2	Q9B345	Q9B345 clostridium
10	1270	50.3	448	5	Q9B067	Q9B067 copiotermes
11	1265.8	50.3	719	2	Q9A318	Q9A318 clostridium
12	1266.7	49.7	466	2	Q9B345	Q9B345 clostridium
13	1247.8	49.0	1070	2	Q65985	Q65985 synchocystis
14	1239.6	48.9	448	5	Q9B067	Q9B067 copiotermes
15	1222.4	48.4	448	5	Q9B067	Q9B067 copiotermes
16	1219.4	48.3	448	5	Q9B067	Q9B067 copiotermes
17	1219.4	48.3	448	5	Q9B067	Q9B067 copiotermes
18	1219.4	48.3	448	5	Q9B067	Q9B067 copiotermes
19	1219.4	48.3	448	5	Q9B067	Q9B067 copiotermes

20	1219.4	48.3	448	5	Q9B022	Q9B022 copiotermes
21	1211	46.0	117	5	Q9B016	Q9B016 bacillus p
22	1209.8	47.9	448	5	Q9B016	Q9B016 bacillus p
23	1195.2	47.3	448	5	Q9B016	Q9B016 bacillus p
24	1195.1	47.3	448	5	Q9B016	Q9B016 bacillus p
25	1194.1	46.5	448	5	Q9B016	Q9B016 bacillus p
26	1166.7	46.2	448	5	Q9B016	Q9B016 bacillus p
27	1164.6	46.1	448	5	Q9B016	Q9B016 bacillus p
28	1159	45.9	448	5	Q9B016	Q9B016 bacillus p
29	1153	45.7	448	5	Q9B016	Q9B016 bacillus p
30	1152.6	45.6	448	5	Q9B016	Q9B016 bacillus p
31	1151.1	45.6	448	5	Q9B016	Q9B016 bacillus p
32	1149.4	45.5	448	5	Q9B016	Q9B016 bacillus p
33	1144	45.3	448	5	Q9B016	Q9B016 bacillus p
34	1108.6	43.9	448	5	Q9B016	Q9B016 bacillus p
35	1091.4	43.2	448	5	Q9B016	Q9B016 bacillus p
36	1085.1	43.0	448	5	Q9B016	Q9B016 bacillus p
37	1080.5	42.8	448	5	Q9B016	Q9B016 bacillus p
38	1078.9	42.7	448	5	Q9B016	Q9B016 bacillus p
39	1077.5	42.7	448	5	Q9B016	Q9B016 bacillus p
40	1077.3	42.7	448	5	Q9B016	Q9B016 bacillus p
41	1074.6	42.6	448	5	Q9B016	Q9B016 bacillus p
42	1074	42.5	448	5	Q9B016	Q9B016 bacillus p
43	1073.2	42.5	448	5	Q9B016	Q9B016 bacillus p
44	1072.2	42.5	448	5	Q9B016	Q9B016 bacillus p
45	1069.2	42.3	448	5	Q9B016	Q9B016 bacillus p

#### ALIGNMENTS

Result ID	Query Match	Length	DB	ID	Description
1	86.1	65	2	Q9B022	Q9B022 copiotermes
2	75.0	65	2	Q9B016	Q9B016 bacillus p
3	59.6	937	2	Q9A311	Q9A311 bacillus sp
4	54.4	847	2	Q9A318	Q9A318 clostridium
5	59.5	1711	2	P96311	P96311 anaerobell
6	58.0	715	2	Q65987	Q65987 clostridium
7	55.9	1751	2	Q9A004	Q9A004 bacillus p
8	54.7	742	2	Q9B345	Q9B345 clostridium
9	52.9	737	2	Q9B345	Q9B345 clostridium
10	50.3	448	5	Q9B067	Q9B067 copiotermes
11	50.3	719	2	Q9A318	Q9A318 clostridium
12	49.7	466	2	Q9B345	Q9B345 clostridium
13	49.0	1070	2	Q65985	Q65985 synchocystis
14	48.9	448	5	Q9B067	Q9B067 copiotermes
15	48.4	448	5	Q9B067	Q9B067 copiotermes
16	48.3	448	5	Q9B067	Q9B067 copiotermes
17	48.3	448	5	Q9B067	Q9B067 copiotermes
18	48.3	448	5	Q9B067	Q9B067 copiotermes
19	48.3	448	5	Q9B067	Q9B067 copiotermes

[illegible]

Only Mut. 75.08; Score 1993.4; Ols 2; Length 659;  
best Local Similarity 70.68; Prod. No. 8, 46-49;  
Mut. chos. 41; Conservative 58; Mismatches 64; Indels 16; Gaps 9;  
4 EF. . . . Y. . . . . HNYALLQKSLLEVAHNSRITFNRIMNRDLSGLDQVGLPTGG 56

[illegible]

RESULT	3			
092411				
TD	092411	PRELIMINARY:	PRT:	997 AA.
AC	092411:			
DT	01-MAY-1999 (IREMBREL, 10, Created)			
DT	01-MAY-1999 (IREMBREL, 10, Last sequence update)			
DT	01-JUN-2001 (IREMBREL, 17, Last annotation update)			
DE	CELLULASE PROTEINASE (EC 3.2.1.4),			
GN	CELH.			
OS	Bacillus sp., BP-23.			
OC	Bacteria: Firmicutes: Bacillus/Clostridium group;			
GC	Bacillus/Staphylococcus group: Bacillus.			
OX	NCBI_taxid:89769;			
KN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-BP-23;			
KA	Diaz P., Patel X., Prim N., Blanco A., Pastor F.J.?			
RT	"Isolation and characterization of a multipolymeric extracellular			
BT	Bacillus sp., BP-23."			
ST	Submitted (MAY-1999) to the Protein Data Bank.			
OR	EMBL, AJ13614; CAB4941.1; ...			
OR	HEAT: P24221; ...			
OR	InterPro: IPR001956; CHD_3.			
OR	InterPro: IPR003661; FN_111.			
OR	InterPro: IPR001701; Glyco_Hydro_9.			
OR	InterPro: IPR000566; Lipid_CyclFABH.			
OR	Proam: PF00942; CHD_3; ...			
OR	Proam: PF00941; Hs3_2; ...			
OR	Proam: PF00759; Glyco_Hydro_9; ...			
OR	Prodom: P0001947; CHD_3; ...			
OR	SMART: SM00060; FN3_2.			
OR	PROSITE: PS00592; GLYCASYL_HYDROL_F9_1; ...			
OR	PROSITE: PS00698; GLYCASYL_HYDROL_F9_2; ...			
OR	PROSITE: PS00213; LIPOLYTIN: MNKNMN_1.			
OR	Glycosidase: Hydrolase; Signal			
FT	SIGNAL	1	34	potential
FT	SEQUENCE	997 AA:	199927 BP:	1209411966410629 Cpe964;

Query Match	69.68;	Score	1757.2;	Length	997;
Best Local Similarity	65.06;	Prod. No.	9.46-64;		













D8 HSSP: p26221; 1TP4.  
 D8 InterPro: IPR001919; GH2\_2.  
 D8 Pfam: PF00553; GH2\_2; 1.  
 D8 Pfam: PF00759; Glyco\_hydro\_9; 1.  
 D8 PROSITE: PS00698; GLYCOSYL\_HYDROL\_F9\_2; 1.  
 KW Complete proteome.  
 SQ SOURCE: 1070 AA; 112131 MW; 914805060FC69A CPY64;

Query Match 49.0% Score 1227.9; DR 2; Length 1070.  
 Best Local Similarity 41.6% Pred. No. 870-19;  
 Matches 251; Conserved 65; Mismatches 105; Indels 18; Gaps 52.

QY 1 AS-----APE-----Y-----P-----7  
 DB 505 ASLADSSVVEVFNPTGTAALANDCATMLLEFGGIVGQSTSGCTGTPTNPRF 564  
 QY H-----HNAHLQKSLIYFQGRGPRFENS PLNRGDSGL 43  
 DB 565 TDPIINPNIYVDIPDALANGHNHNGEALQSELYEANKSGDLESTRIDWDSGL 624  
 QY 44 EHKRD-----VG--LDLGSWDADHVKFGLPMAYSAALISL-SVEYED 87  
 DB 625 KDKKQGYFGSSSSNIGALSLITGTYHEATHEHCHLGLASLILLAWV-V-LTITG 582  
 QY 88 YKPSGLDIALD---NFKATDYFAH-T-ADYELAG--GVNGLDIAWV GF 134  
 DB 684 YGSGQMD---DLATLPMETDILKAVTNAN---GEVEFVAGVNASDHSIWSAF 736  
 QY 145 AFWPMRPAYKTIAQTPNSDIAGCTAAALASASTITPT--GSSEKLLIAIKQIDFA 193  
 DB 747 FSGTAPAPMAVATANKPSSDVAGASAAALAAASTIFPALEFPAIDELLYAGSLTFA 795  
 QY 194 DRTGKASGCTIAGQYNSGSCFELTGCWAWLYAT---EEOGYLTKALASV--S 246  
 DB 796 DTYRKYSOSTPEVENYNSWSYELAYGAALSPAVNSAGDPSAVIGAL-NLYNS 854  
 QY 247 DWDVAMRYR WTLSKTYTANGLIAGLT NISAYE--VEARLQVNS-QYGRSS- 362  
 DB 855 DIGNLS---KNTINMDASGVAVLLAQDTGNOA--TKQNTWLLAWV---NSTD 903  
 QY 403 LKRTYTTQGLAMLEPQWSTPYASNAFLAVYSIW-V-TEKAPRYDFAVQ 257  
 DB 904 GVG-L--TDCGLPELISQWSTPYAANTAMLAAYSGSLTDPK---VAGLA--GLTIVY 956  
 QY 458 MLDNIVGSGSVYVYKRP PKRPHITAG--SW--ANGVNPVNHHTLYGALVSSP- 111  
 DB 956 ILSNPRNASYWGQ-NDFQGPHPRASVQWQGFNP--GLP-N-EHLLFGALVST 1010  
 QY 412 -GHSYED- DTPVASSEVALDYNAFTQVA-FMPSIPEKQVD----LHP- 458  
 DB 1011 AANDSVYNISRD--DYISSEVALDYNAITGALANSVQ-TS-GN-PLTAQLNAPRIS 1065  
 QY 459 -PE 460  
 DB 1066 APV 1068

## RESULT 14

077044 PRELIMINARY; PRI: 448 AA.

AC 077044;  
 DT 01-NOV-1998 (FREMIREL. 08; Created)  
 DT 01-NOV-1998 (FREMIREL. 08; Last sequence update)  
 DT 01-JUN-2001 (FREMIREL. 17; Last annotation update)  
 DB NREG PRECURSOR (EC 3.2.1.4).  
 KW NREG;  
 KW Nasutitermes (Kasapoensis;  
 KW Parityx; Molitor; Arthropoda; Tracheata; Hexapoda; Insecta;  
 KW Polyvala; Molitor; Orthopteroidea; Dictyoptera; Isoptera;  
 KW Termitidae; Nasutitermitinae; Nasutitermes;  
 KW NCHL\_TaxID 62960;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Tokida C., In N., Matsuda S., Slagter M., Matsuda T., Noda H.,  
 RT "Protein and distribution of Metazoan Cellulases in Termites.";  
 RL Submitted (Apr-1998) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Tokida C., In N., Matsuda H., Slagter M., Matsuda T., Noda H.,  
 RT "Metazoan cellulase gene from termites: Intron/exon structures and  
 RL sites of expression.";  
 RL Submitted (Oct 1998) to the EMBL/GenBank/DBJ databases.

DR EMBL: AB019272; J0433708.1;  
 DR EMBL: AB019446; J0433708.1;  
 DR HSSP: p26221; 1TP4.  
 DR InterPro: IPR001701; Glyco\_hydro\_9.  
 DR Pfam: PF00759; Glyco\_hydro\_9; 1.  
 DR PROSITE: PS00698; GLYCOSYL\_HYDROL\_F9\_2; 1.  
 KW Signal; hydrolase; glycosidase.  
 FT SIGNAL: 1-16  
 SQ SOURCE: 448 AA; 49404 MW; PF0080698060FC69A CPY64;

Query Match 48.7% Score 1229.5; DR 5; Length 448;  
 Best Local Similarity 48.0% Pred. No. 546-21;  
 Matches 237; Conserved 62; Mismatches 92; Indels 105; Gaps 30;

QY 2 SA---LPHRTALQKSLIYFQGRGPRFENS PLNRGDSGL 43  
 DB 9 SALALFQAV--GVYVTEPLSLIYFQGRGPRFENS PLNRGDSGL 43  
 QY 56 GWTATITVPEL--GAYSAALISL-SVEYED 87  
 DB 66 GYELAFYKPSHPRAYALVLAWDLIR-FASISALD---GVNGLDIAWV GF 134  
 QY 112 HPAFLYLVGSH ALILHAWG FENYHREAFELHAGTQSGAAGAAALASAI 169  
 DB 122 HTEGSEVYVSGIA LQAWSP EGTMTATVHIDSSGSLAAGAAALASAI 179  
 QY 177 TTSVTEFLAMF-LYLMGYSCH-LIILAGLYNS-TRILGSAVVA 229  
 DB 180 VPEVMTVSNMILHAPGLDFAHYEKEYSSTYDANRYAG AYRGLHVAWAAV 248  
 QY 220 LATHNGYTPKAVAGV--WEDARDTSLDQVYVAGLADIAH 274  
 DB 239 KATPDYLYGK EELTETGLQIMDQ--GKMSKVS-VYVGLAKLIRGA 288  
 QY 279 DSEVKEVDEMLDWTYSERSTETATYTGAMALAMNKAAGAAAFV 344  
 DB 289 KQV VQS--V-VYVIRHQ--TIRKLTTCQWCHIRAHAAFTMLDA-- 442  
 QY 335 YELWITE--KARETHFAVGL LETHGAGVLSVVS-TRGTFHMGAGS 488  
 DB 333 -----DELGLASSYVGA GTEIDVALGQ GSEVYVGNSTPHHNS-SC 480  
 QY 389 WAGRNITE NHHTLYGALVGSIGLSTAGATTAAGAAALVAPRAVQ 439  
 DB 381 PRPATGDM-NITRSHREYV HESGALVGSIGLSTAGATTAAGAAALVAPRAVQ 439  
 QY 440 RVAKMTY--LFSKQ 452  
 DB 436 -----FQSALAAVAGY 448

## RESULT 15

077045 PRELIMINARY; PRI: 448 AA.

AC 077045;  
 DT 01-NOV-1998 (FREMIREL. 08; Created)  
 DT 01-NOV-1998 (FREMIREL. 08; Last sequence update)  
 DT 01-JUN-2001 (FREMIREL. 17; Last annotation update)  
 DB NREG PRECURSOR (EC 3.2.1.4).  
 KW NREG;  
 KW Nasutitermes (Walker);

CG Burkaryat; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 CG Pterygota; Neoptera; Orthoptera; Dermaptera; Isoptera;  
 CG Termitidae; Nasutitermitidae; Nasutitermes;  
 CG Nchi\_taxid=76108;  
 KN [1]  
 RP SEQUENCE FROM N.A.  
 PA Tokuda G., Lo N., Marashe H., Saffor M., Matsumoto T., Noda H.;  
 KI "Origin and Distribution of Molluscan Cellulases in Termites";  
 RL Submitted (Apr-1998) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL: AB013273; BAA33709.1; -  
 DR HSSP: P26221; 1TF4.  
 DR InterPro: IPR01701; Glyco\_hydro\_9.  
 DR Pfam: PF00759; Glyco\_hydro\_9; 1.  
 DR PROSITE: PS00698; GLYCOSYL\_HYDROL\_P9\_2; 1.  
 KM Signal: Hydrolase; Glycosidase.  
 FT SIGNAL: 1  
 ST SPONDINE 448 AA; 49454 MW; 97AFCD0108EP9A8 Cn664;

Query Match 48 48; Score 1222.4; DB 5; Length 448;

Best Local Similarity 47.48; Proc. No. 8; to 21; Indels 107; Gaps 49;

Matches 246; Conservative 66; Mismatches 90; Indels 107; Gaps 49;  
 QY 2 SA- EHYRNVALLKSLIYLAKGRLHNSGNNWGGSLH; GRDVGLDLDG 55  
 DB 9 SALALVAAV-LYKQVPSITFYALQSDIPAKGVTKKISAI NNGRPQ-QDLDLG 65  
 QY 56 QMTLAA NVRFH PAAVSAH SSVVFHFA TFSGLTAAH N--FWALVPLAA 111  
 DB 66 QYTAADLVKTFEPMAYTAVI AWHLIEF LADSSVADLQ--TSPKAVVAAVDFEA 121  
 QY 112 HFAVTHLVNVRGALDHWAG IAVYHKKGAATLARTPSLADITAAALASSTI 170  
 DB 122 HFGVNIYVGVGVGVHAWGRI ESMHMAHAKRIH ESRPSLADITAAALASSTV 180  
 QY 171 PPTPTGVSEFET IAAKALVYFAVYFVGVV TIDVGVYRSGVYPTLTWZAVDYL 230  
 DB 181 PFTV-LTVSYRI THAFETIAAGHFEVYSGITIAHGTAS AVEEDLYWAAADLYR 239  
 QY 221 ATEEGVGVVALASV EHWG EFAHRTHW TLEWEL VTYGAGLTLAALTHSLVSG 285  
 DB 240 ATRNSSTNFA-FSTVWFTQ--N--WVSGHWVFS VAVLAKETN- EQ 286  
 QY 286 VERNLYWGH QYSHRSLEHITY TTHLAWIDWMSLKVASNAFL AF 344  
 DB 297 FVKTTEV-- VYV--VY--L FNLDTI HMTHLHAAHATITLWMA 342  
 QY 444 VYQAWG TTRKSTFEFAVPT FEMDANKVSEVYVYKNGVGHFHRTAHGS 408  
 DB 434 --ADHLIS--ASSYKQFA--QIQIDVALDNG--GRSEVYGRGSDPTREHRRSS--S 479  
 QY 489 - - - - - WAKHNYHE RHHTLYGAVNATVAGNGGIRGATITVAAGNFAALYNAFT 448  
 DB 480 QPVAATIDW-RETFETINR RYLSDAVQDITG--NGVYDNRGVHREVAIDINA-- 444  
 QY 439 GNVAKKMPG-- --LEQKCH 452  
 DB 435 G-- -- PVSALALVALGY 448

Search completed: March 5, 2002, 08:00:06  
 Job time: 213 sec

